

A. Marschel

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RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/446,415

DATE: 11/16/2000  
TIME: 19:13:40

Input Set : A:\11034WO1.SEQ.txt  
Output Set: N:\CRF3\11162000\I446415.raw

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:

6 (i) APPLICANT: Beamer, Lesa J., Carroll, Stephen F., Eisenber, David  
8 (ii) TITLE OF INVENTION: Bactericidal/Permeability-Increasing Protein:  
9 Crystallization, X-Ray Diffraction, Three-Dimensional Structure  
10 Determination, Rational Drug Design and Molecular Modeling of  
11 Related Proteins

13 (iii) NUMBER OF SEQUENCES: 2

15 (iv) CORRESPONDENCE ADDRESS:

16 (A) ADDRESSEE: McAndrews, Held & Malloy  
17 (B) STREET: 500 West Madison, 34th Floor  
18 (C) CITY: Chicago  
19 (D) STATE: Illinois  
20 (E) COUNTRY: United States of America  
21 (F) ZIP: 60661

23 (v) COMPUTER READABLE FORM:

24 (A) MEDIUM TYPE: Floppy disk  
25 (B) COMPUTER: IBM PC compatible  
26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

29 (vi) CURRENT APPLICATION DATA:

30 (A) APPLICATION NUMBER: US/09/446,415  
31 (B) FILING DATE: 19-Jul-2000

37 (C) CLASSIFICATION:

34 (vii) PRIOR APPLICATION DATA:

35 (A) APPLICATION NUMBER:

36 (B) FILING DATE:

39 (viii) ATTORNEY/AGENT INFORMATION:

40 (A) NAME: McNicholas, Janet M.

41 (B) REGISTRATION NUMBER: 32,918

42 (C) REFERENCE/DOCKET NUMBER: 11034US01;100-248

45 (ix) TELECOMMUNICATION INFORMATION:

46 (A) TELEPHONE: 312/707-8889

47 (B) TELEFAX: 312/707-9155

48 (C) TELEX:

51 (2) INFORMATION FOR SEQ ID NO: 1:

53 (i) SEQUENCE CHARACTERISTICS:

54 (A) LENGTH: 1813 base pairs  
55 (B) TYPE: nucleic acid  
56 (C) STRANDEDNESS: single  
57 (D) TOPOLOGY: linear

59 (i.i) MOLECULE TYPE: cDNA

62 (i.x) FEATURE:

63 (A) NAME/KEY: CDS

64 (B) LOCATION: 31..1491

66 (i.x) FEATURE:

67 (A) NAME/KEY: mat\_peptide

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Input Set : A:\11034W01.SEQ.txt  
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68	(B) LOCATION: 124..1491	
70	(ix) FEATURE:	
71	(A) NAME/KEY: misc_feature	
73	(D) OTHER INFORMATION: "rBPI"	
76	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:	
78	CAGGCCCTGCA GGTGGCGCA CCTCTGGACG ATG AGA GAG AAC ATG GCC AGG GGC	54
79	Met Arg Glu Asn Met Ala Arg Gly	
80	-31 -30 -25	
82	CCT TGC AAC GCG CCG AGA TGG GTG TCC CTG ATG GTG CTC GTC GCC ATA	102
83	Pro Cys Asn Ala Pro Arg Trp Val Ser Leu Met Val Leu Val Ala Ile	
84	-20 -15 -10	
86	GGC ACC GCC GTG ACA GCG GCC GTC AAC CCT GGC GTC GTG GTC AGG ATC	150
87	Gly Thr Ala Val Thr Ala Ala Val Asn Pro Gly Val Val Val Arg Ile	
88	-5 1 5	
90	TCC CAG AAG GGC CTG GAC TAC GCC AGC CAG CAG GGG AGC GCC GCT CTG	198
91	Ser Gln Lys Gly Leu Asp Tyr Ala Ser Gln Gln Gly Thr Ala Ala Leu	
92	10 15 20 25	
94	CAG AAG GAG CTG AAG AGG ATC AAG ATT CCT GAC TAC TCA GAC AGC TTT	246
95	Gln Lys Glu Leu Lys Arg Ile Lys Ile Pro Asp Tyr Ser Asp Ser Phe	
96	30 35 40	
98	AAG ATC AAG CAT CTT GGG AAG GGG CAT TAT AGC TTTC TAC AGC ATG GAC	294
99	Lys Ile Lys His Leu Gly Lys Gly His Tyr Ser Phe Tyr Ser Met Asp	
100	45 50 55	
102	ATC CGT GAA TTC CAG CTT CCC AGT TCC CAG ATA AGC ATG GTG CCC AAT	342
103	Ile Arg Glu Phe Gln Leu Pro Ser Ser Gln Ile Ser Met Val Pro Asn	
104	60 65 70	
106	GTG GGC CTT AAG TTC TCC ATC AGC AAC GCC AAT ATC AAG ATC AGC GGG	390
107	Val Gly Leu Lys Phe Ser Ile Ser Asn Ala Asn Ile Lys Ile Ser Gly	
108	75 80 85	
110	AAA TGG AAG GCA CAA AAG AGA TTC TTA AAA ATG AGC GGC AAT TTT GAC	438
111	Lys Trp Lys Ala Gln Lys Arg Phe Leu Lys Met Ser Gly Asn Phe Asp	
112	90 95 100 105	
114	CTG AGC ATA GAA GGC ATG TCC ATT TCG GCT GAT CTG AAG CTG GGC AGT	486
115	Leu Ser Ile Glu Gly Met Ser Ile Ser Ala Asp Leu Lys Leu Gly Ser	
116	110 115 120	
118	AAC CCC ACG TCA GGC AAG CCC ACC ATC ACC TGC TCC AGC TGC AGC AGC	534
119	Asn Pro Thr Ser Gly Lys Pro Thr Ile Thr Cys Ser Ser Cys Ser Ser	
120	125 130 135	
122	CAC ATC AAC AGT GTC CAC GTG CAC ATC TCA AAG AGC AAA GTC GGG TGG	582
123	His Ile Asn Ser Val His Val Ile Ser Lys Ser Lys Val Gly Trp	
124	140 145 150	
126	CTG ATC CAA CTC TTC CAC AAA AAA ATT GAG TCT GCG CTT CGA AAC AAG	630
127	Leu Ile Gln Leu Phe His Lys Lys Ile Glu Ser Ala Leu Arg Asn Lys	
128	155 160 165	
130	ATG AAC AGC CAG GTC TGC GAG AAA GTG ACC AAT TCT GTA TCC TCC AAG	678
131	Met Asn Ser Gln Val Cys Glu Lys Val Thr Asn Ser Val Ser Lys	
132	170 175 180 185	
134	CTG CAA CCT TAT TTC CAG ACT CTG CCA GTC ATG ACC AAA ATA GAT TCT	726
135	Leu Gln Pro Tyr Phe Gln Thr Leu Pro Val Met Thr Lys Ile Asp Ser	

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136	190	195	200	
138	GTC CCT CGA ATC AAC TAT CGT CTC GTG GCA CCT CCA GCA ACC ACG GCT			774
139	Val Ala Gly Ile Asn Tyr Gly Leu Val Ala Pro Pro Ala Thr Thr Ala			
140	205	210	215	
142	GAG ACC CTG GAT CTA CAG ATG AAG GGG GAG TTT TAC ACT GAG AAC CAC			822
143	Glu Thr Leu Asp Val Gln Met Lys Gly Glu Phe Tyr Ser Gln Asn His			
144	220	225	230	
146	CAC AAT CCA CCT CCC TTT GCT CCA CCA GTG ATG GAG TTT CCC GCT GCC			870
147	His Asn Pro Pro Pro Phe Ala Pro Pro Val Met Glu Phe Pro Ala Ala			
148	235	240	245	
150	CAT GAC CGC ATG GTC TAC CGT GGC CTC TCA GAC TAC TTC TTC AAC ACA			918
151	His Asp Arg Met Val Tyr Leu Gly Leu Ser Asp Tyr Phe Phe Asn Thr			
152	250	255	260	265
154	GCC GGG CTT GTC TAC CAA GAG GCT GGG GTC TTG AAG ATG ACC CTT AGA			966
155	Ala Gly Leu Val Tyr Gln Glu Ala Gly Val Leu Lys Met Thr Leu Arg			
156	270	275	280	
158	GAT GAC ATG ATT CCA AAG GAG TCC AAA TTT CGA CTG ACA ACC AAG TTC			1014
159	Asp Asp Met Ile Pro Lys Glu Ser Lys Phe Arg Leu Thr Lys Phe			
160	285	290	295	
162	TTT GGA ACC TTC CTA CCT GAG GTG GCC AAG AAG TTT CCC AAC ATG AAG			1062
163	Phe Gly Thr Phe Leu Pro Glu Val Ala Lys Lys Phe Pro Asn Met Lys			
164	300	305	310	
166	ATA CAG ATC CAT GTC TCA GCC TCC ACC CCG CCA CAC CTG TCT GTG CAG			1110
167	Ile Gln Ile His Val Ser Ala Ser Thr Pro Pro His Leu Ser Val Gln			
168	315	320	325	
170	CCC ACC GGC CTT ACC TTC TAC CCT GCC GTG GAT GTC CAG GCC TTT GCC			1158
171	Pro Thr Gly Leu Thr Phe Tyr Pro Ala Val Asp Val Gln Ala Phe Ala			
172	330	335	340	345
174	GTC CTC CCC AAC TCC TCC CTG GCT TCC CTC TTC CTG ATT GGC ATG CAC			1206
175	Val Leu Pro Asn Ser Ser Leu Ala Ser Leu Phe Leu Ile Gly Met His			
176	350	355	360	
178	ACA ACT GGT TCC ATG GAG GTC AGC GCC GAG TCC AAC AGG CTT GTT GGA			1254
179	Thr Thr Gly Ser Met Glu Val Ser Ala Glu Ser Asn Arg Leu Val Gly			
180	365	370	375	
182	GAG CTC AAG CTG GAT AGG CTG CTC CTG GAA CTG AAG CAC TCA AAT ATT			1302
183	Glu Leu Lys Leu Asp Arg Leu Leu Glu Leu Lys His Ser Asn Ile			
184	380	385	390	
186	GGC CCC TTC CCG GTT GAA TTG CTG CAG GAT ATC ATG AAC TAC ATT GTC			1350
187	Gly Pro Phe Pro Val Glu Leu Leu Gln Asp Ile Met Asn Tyr Ile Val			
188	395	400	405	
190	CCC ATT CTT GTG CTG CCC AGG GTT AAC GAG AAA CTA CAG AAA GGC TTC			1398
191	Pro Ile Leu Val Leu Pro Arg Val Asn Glu Lys Leu Gln Lys Gly Phe			
192	410	415	420	425
194	CCT CTC CCG ACG CCG GCC AGA GTC CAG CTC TAC AAC GTC GTG CTT CAG			1446
195	Pro Leu Pro Thr Pro Ala Arg Val Gln Leu Tyr Asn Val Val Leu Gln			
196	430	435	440	
198	CCT CAC CAG AAC TTC CTG CTG TTC CGT GCA GAC GTT GTC TAT AAA			1491
199	Pro His Gln Asn Phe Leu Phe Gly Ala Asp Val Val Tyr Lys			
200	445	450	455	

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202	TGAAGGCACC	AGGGGTGCCG	GGGGCTGTCA	GCCGCACCTG	TTCCTGATGG	GCTGTGGGGC	1551
204	ACCGCTGCC	TTTCCCCAGG	GAATCCTCTC	CAGATCTAA	CCAAGAGCCC	CTTGCAAACT	1611
206	TCTTCGAETC	AGATTCAAGA	ATGATCTAAA	CACGAGGAAA	CATTATTCA	TGGAAAAGTG	1671
208	CATGCTGTGT	ATTTTAGGGA	TTATGAGCTT	CTTTCAGGG	CTAACGGC'GC	AGAGATAATT	1731
210	CCTCCAGGAA	TCCGTGTTC	ATTGTAACCA	AGAAAATTCC	ATTTGTGCTT	CATGAAAAAA	1791
212	AACTTCTGGT	TTTTTCATG	TG				1813
215	(2) INFORMATION FOR SEQ ID NO: 2:						
217	(i) SEQUENCE CHARACTERISTICS:						
218	(A) LENGTH: 487 amino acids						
219	(B) TYPE: amino acid						
220	(D) TOPOLOGY: linear						
222	(ii) MOLECULE TYPE: protein						
224	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:						
226	Met Arg Glu Asn Met Ala Arg Gly Pro Cys Asn Ala Pro Arg Trp Val						
227	-31 -30	-25	-20				
229	Ser Leu Met Val Leu Val Ala Ile Gly Thr Ala Val Thr Ala Ala Val						
230	-15	-10	-5		1		
232	Asn Pro Gly Val Val Val Arg Ile Ser Gln Lys Gly Leu Asp Tyr Ala						
233	5	10	15				
235	Ser Gln Gln Gly Thr Ala Ala Leu Gln Lys Glu Leu Lys Arg Ile Lys						
236	20	25	30				
238	Ile Pro Asp Tyr Ser Asp Ser Phe Lys Ile Lys His Leu Gly Lys Gly						
239	35	40	45				
241	His Tyr Ser Phe Tyr Ser Met Asp Ile Arg Glu Phe Gln Leu Pro Ser						
242	50	55	60		65		
244	Ser Gln Ile Ser Met Val Pro Asn Val Gly Leu Lys Phe Ser Ile Ser						
245	70	75	80				
247	Asn Ala Asn Ile Lys Ile Ser Gly Lys Trp Lys Ala Gln Lys Arg Phe						
248	85	90	95				
250	Leu Lys Met Ser Gly Asn Phe Asp Leu Ser Ile Glu Gly Met Ser Ile						
251	100	105	110				
253	Ser Ala Asp Leu Lys Leu Gly Ser Asn Pro Thr Ser Gly Lys Pro Thr						
254	115	120	125				
256	Ile Thr Cys Ser Ser Cys Ser Ser His Ile Asn Ser Val His Val His						
257	130	135	140		145		
259	Ile Ser Lys Ser Lys Val Gly Trp Leu Ile Gln Leu Phe His Lys Lys						
260	150	155	160				
262	Ile Glu Ser Ala Leu Arg Asn Lys Met Asn Ser Gln Val Cys Glu Lys						
263	165	170	175				
265	Val Thr Asn Ser Val Ser Ser Lys Leu Gln Pro Tyr Phe Gln Thr Leu						
266	180	185	190				
268	Pro Val Met Thr Lys Ile Asp Ser Val Ala Gly Ile Asn Tyr Gly Leu						
269	195	200	205				
271	Val Ala Pro Pro Ala Thr Thr Ala Glu Thr Leu Asp Val Gln Met Lys						
272	210	215	220		225		
274	Gly Glu Phe Tyr Ser Glu Asn His His Asn Pro Pro Pro Phe Ala Pro						
275	230	235	240				
277	Pro Val Met Glu Phe Pro Ala Ala His Asp Arg Met Val Tyr Leu Gly						
278	245	250	255				

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Input Set : A:\11034W01.SEQ.txt  
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280 Leu Ser Asp Tyr Phe Phe Asn Thr Ala Gly Leu Val Tyr Gln Glu Ala  
281 260 265 270  
283 Gly Val Leu Lys Met Thr Leu Arg Asp Asp Met Ile Pro Lys Glu Ser  
284 275 280 285  
286 Lys Phe Arg Leu Thr Thr Lys Phe Phe Gly Thr Phe Leu Pro Glu Val  
287 290 295 300 305  
289 Ala Lys Lys Phe Pro Asn Met Lys Ile Gln Ile His Val Ser Ala Ser  
290 310 315 320  
292 Thr Pro Pro His Leu Ser Val Gln Pro Thr Gly Leu Thr Phe Tyr Pro  
293 325 330 335  
295 Ala Val Asp Val Gln Ala Phe Ala Val Leu Pro Asn Ser Ser Leu Ala  
296 340 345 350  
298 Ser Leu Phe Leu Ile Gly Met His Thr Thr Gly Ser Met Glu Val Ser  
299 355 360 365  
301 Ala Glu Ser Asn Arg Leu Val Gly Glu Leu Lys Leu Asp Arg Leu Leu  
302 370 375 380 385  
304 Leu Glu Leu Lys His Ser Asn Ile Gly Pro Phe Pro Val Glu Leu Leu  
305 390 395 400  
307 Gln Asp Ile Met Asn Tyr Ile Val Pro Ile Leu Val Leu Pro Arg Val  
308 405 410 415  
310 Asn Glu Lys Leu Gln Lys Gly Phe Pro Leu Pro Thr Pro Ala Arg Val  
311 420 425 430  
313 Gln Leu Tyr Asn Val Val Leu Gln Pro His Gln Asn Phe Leu Leu Phe  
314 435 440 445  
316 Gly Ala Asp Val Val Tyr Lys  
317 450 455

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VERIFICATION SUMMARY DATE: 11/16/2000  
PATENT APPLICATION: US/09/446,415 TIME: 19:13:41

Input Set : A:\11034W01.SEQ.txt  
Output Set: N:\CRF3\11162000\I446415.raw

L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]